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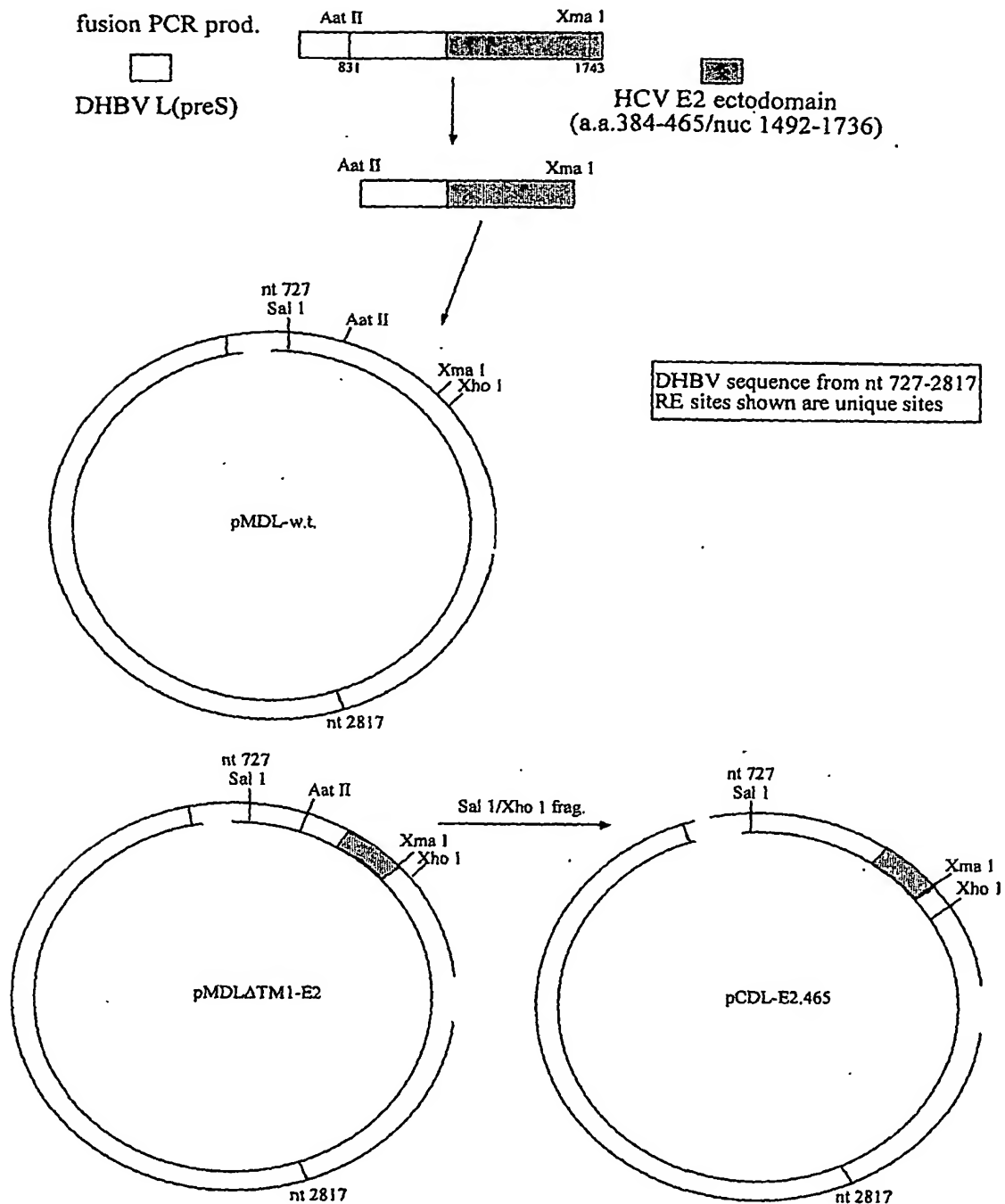
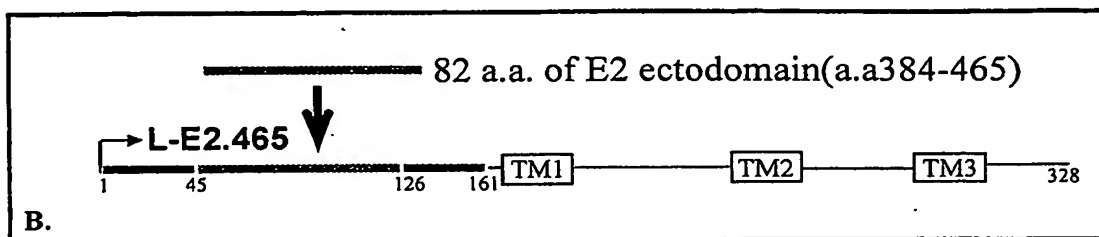
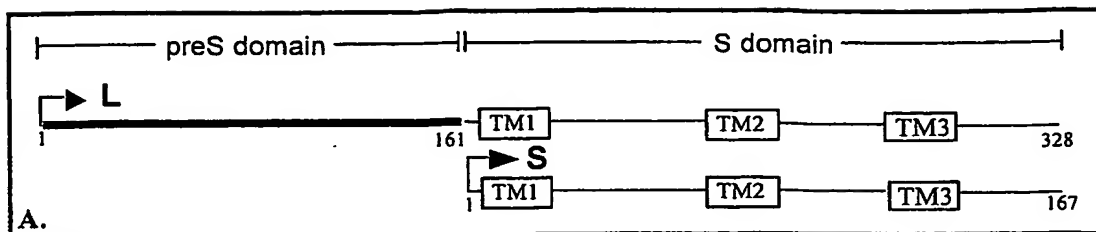


FIGURE 1

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C. L-E2.465 chimera is translocated across the ER membrane

trypsin	-	+	+
NP-40	-	-	+

L-E2.465 —

S —

microsomes: protease protection assay

D. L-E2.465 chimera is assembled into particles

L-E2.465 —

S —

particles purified by sedimentation through 20% sucrose

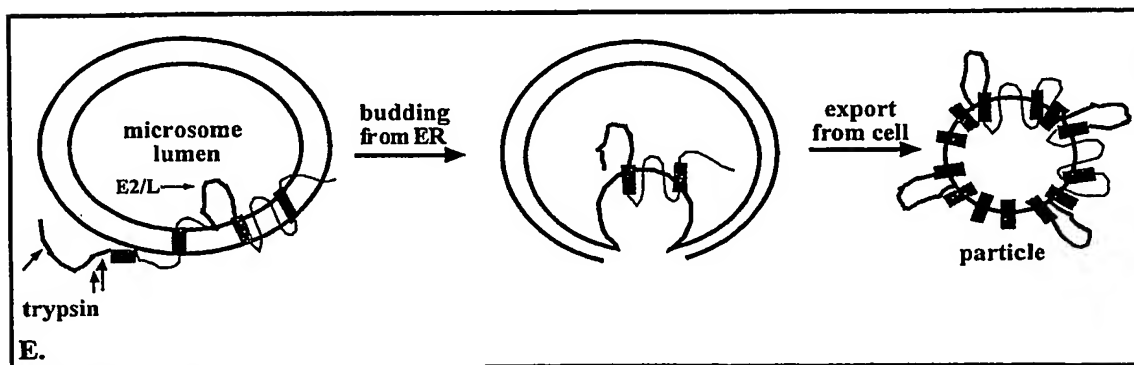


FIGURE 2

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DHBV full genome sequence (US D16 Acc. No. K01839)

1 catgctcatt tgaaagctta tgcaaaaatt aacgaggaat cactggatag ggctaggaga
 61 ttgcttttgt ggcattacaa ctgtttactg tggggagaag ctcaagttac taactatatt
 121 tctcgtttgc gtacttggtt gtcaactcct gagaaatata gaggtagaga tgccccgacc
 181 attgaagcaa tctactagacc aatccagggtg gctcagggag gcagaaaaac aactacgggt
 241 actagaaaac ctcgtggact cgaacctaga agaagaaaag ttaaaaccac agttgtctat
 301 gggagaagac gttcaaagtc ccgggaaagg agagccccta caccccaacg tgcgggctcc
 361 cctctccac gtagttcgag cagccaccat agatctccct cgcctaggaa ataaattacc
 421 tgctaggcat cacttaggta aattgtcagg actatatcaa atgaagggtt gtacttttaa
 481 ccagaatgg aaagtaccag atatttcgga factcatttt aatttagatg tagttaatga
 541 gtgcccttcc cgaaattgga aatatttgac tccagccaaa ttctggccca agagcatttc
 601 ctactttcct gtccaggtag gggtaaacc aaagtatcct gacaatgtga tgcaacatga
 661 atcaatagta ggtaaattatt taaccagggt ctatgaagca ggaatccttt ataagcggat
 721 atctaaacat ttggtcacat ttaaaggta gccttataat tgggaacagc aacacctgtt
 781 caatcaacat cacatttatg atggggcaac atccagcaaa atcaatggac gtcagacgga
 841 tagaaggagg agaaatactg taaaccaac ttgccggaag gatgatccca aaagggactt
 901 tgacatggtc aggcaagttt ccaacactag atcacgtgtt agaccatgtg caaacaatgg
 961 aggagataaa caccctccag aatcagggag cttggcctgc tggggcggga aggagagtag
 1021 gattatcaaa tccgactcct caagagattc ctacgccccca gtggactccc gaggaagacc
 1081 aaaaagcacg cgaagctttt cgccgttacc aagaagaaaag accaccggaa accaccacca
 1141 ttctccgtc tcccctcct cagtgggaagc tacaaccggg ggacgatcca ctctgggaa
 1201 atcagtctct cctcgagact catccgctat accagtcaga accagcgggtg ccagtataa
 1261 aaactcccc cttgaagaag aaaatgtctg gtaccttcgg gggaatacta gctggcctaa
 1321 tcggattact ggtaagcttt ttctgttga taaaaattct agaaatactg aggaggctag
 1381 attggtgggt gatttctctc agttctcaa agggaaaaat gcaatgcgtt ttcaagata
 1441 ctggagccca aatctctcca cattacgtag gatcttgccc gtggggatgc ccaggatttc
 1501 ttggaccta tctcaggctt ttatcatct tctcttaat cctgctagta gcagcaggct
 1561 tgctgtatct gacggacaac ggggttacta tttaggaaa gctccaatgg gcgctggctt
 1621 cagccctttt ctctccatc tcttactac tgccctcgga tccgaaatct ctgctgctt
 1681 taacgtttgg actttcactt atatggatga ctctctctc tgccaccaa acgctcgtca
 1741 ccttaacgca attagccacg ctgtctgctc tttttacaa gagttaggaa taagaataaa
 1801 ctttgacaaa accacgcctt ctccggtgaa tgaataaga ttctcggtt accagattga
 1861 tgaaaatttc atgaagattg aagaagcag atggaaagaa ttaaggactg taatcaagaa
 1921 aataaaagta ggagaatgg atgactggaa atgtattcaa agatttgtgg ggcatttgaa
 1981 tttgttttg cttttacta aaggtaatat tgaaatgtta aaaccaatgt atgctgctat
 2041 tactaacc aa gtaaacttta gcttctctc atcctatagg actttgttat ataaactaac
 2101 aatgggtgtg tgtaaattaa gaataaagcc aaagtctct gtacctttgc cacgtgtagc

FIGURE 3

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2161 tacagatgct accccaacac atggcgcaat atcccatatc accggcgggga ggcagtggt
2221 tgcttttca aaggtcagag atatacatgt tcaggaaacta ttgatgtctt gtttagccaa
2281 gataatgatt aaaccacgtt gtctcttate tgattcaact ttgtttgcc ataagcgta
2341 tcagacgtta ccatggcatt ttgctatgtt ggccaaacaa ttgctcaaac cgatacaatt
2401 gtactttgtc ccgagcaaat ataatcctgc tgacggccca tccaggcaca aacctcctga
2461 ttggacggct ttccataca cccctctctc gaaagcaata tatattccac ataggctatg
2521 tggaacttaa gaattacacc cctctcctc ggagctgctt gccaaaggat cttacgtct
2581 acattgctgt tgctgtgtg gactgtacct ttggtatgta ccattgttta tgattctgc
2641 ttatatatgg atatcaatgc ttctagagcc ttaggcaatg tgtatgatct accagatgat
2701 ttctttccaa aaatagatga tctgtttaga gatgctaaag acgctttaga gccttattgg
2761 aaatcagatt caataaagaa acatgttttg attgcaactc actttgtgga tctcattgaa
2821 gacttctggc agactacaca gggcatgcat gaaatagccg aatcattaag agctgttata
2881 cctcccacta ctactcctgt tccaccgggt tatcttattc agcacgagga agctgaagag
2941 atacctttgg gagatttatt taaacaccaa gaagaaagga tagtaagttt ccaacccgac
3001 tatccgatta cggctagaat t

FIGURE 3 Cont.

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DHBV L sequence (US D16) (start L atg 801; start S atg 1284)

801/1 atg ggg caa cat cca gca aaa tca atg gac gtc aga cgg ata gaa gga gaa gaa ata ctg
 M G Q H P A K S M D V R R I E G G E I L
 861/21 tta aac caa ctt gcc gga agg atg atc cca aaa ggg act ttg aca tgg tca ggc aag ttt
 L N Q Q L A G R M I P K G T L T W S G K F
 921/41 cca aca cta gat cac gtg tta gac cat gtg caa aca atg gag gag ata aac acc ctc cag
 P T L D H V L D H V Q T M E I N T L Q
 981/61 aat cag gga gct tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct
 N Q G A W P A G A G R R V G L S N P T P
 1041/81 caa gag att cct cag ccc cag tgg act ccc gag gaa gac caa aaa gca cgc gaa gct ttt
 Q E I P Q P Q W T P E E D Q K A R E A F
 1101/101 cgc cgt tat caa gaa gaa cca ccg gaa acc acc acc att cct ccg tct tcc cct cct
 R R Y Q E E R P P E T T T I P P S S P P
 1161/121 cag tgg aag cta caa ccc ggg gac gat cca ctc ctg gga aat cag tct ctc ctc gag act
 Q W K L Q P G D D P L L G N Q S L L E T
 1221/141

FIGURE 4

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cat ccg cta tac cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag
 H P L Y Q S E P A V P V I K T P P L K K
 1281/161
 aaa atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg gta agc ttt
 K M S G T F G I L A G L I G L L V S F
 1341/181
 ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta gat tgg tgg att tct ctc
 F L L I K I L E I L R R L D W W I S L
 1401/201
 agt tct cca aag gga aaa atg caa tgc gct ttc caa gat act gga gcc caa atc tct cca
 S S P K G K M Q C A F Q D T G A Q I S P
 1461/221
 cat tac gta gga tct tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt
 H Y V G S C P W G C P G F L W T Y L R L
 1521/241
 ttt atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg acg gac aac
 F I I F L L I L L V A A G L L Y L T D N
 1581/261
 ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc tca gcc ctt ttc tcc atc
 G S T I L G K L Q W A S V S A L F S I
 1641/281
 tct tca cta ctg ccc tcg gat ccg aaa tct ctc gtc gct tta acg ttt gga ctt tca ctt
 S S L L P S D P K S L V A L T F G L S L
 1701/301
 1731/311

FIGURE 4 Cont.

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ata tgg atg act tcc tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg
I W M T S S S S A T Q T L V T L A T
1761/321
ctg tct gct ctt ttt tac aag agt tag
L S A L F Y K S *
1791/331

```

FIGURE 4 Cont.

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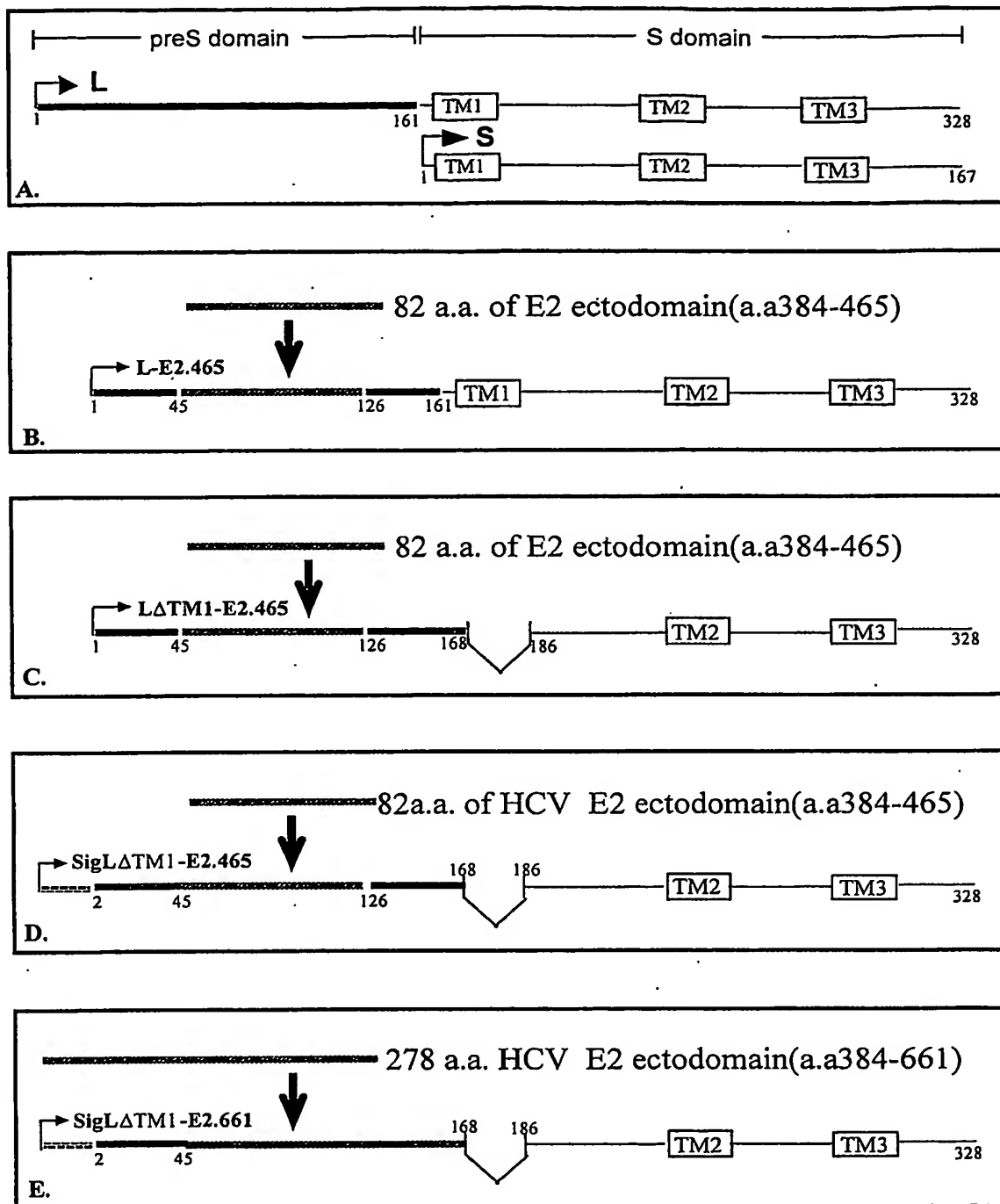


FIGURE 5

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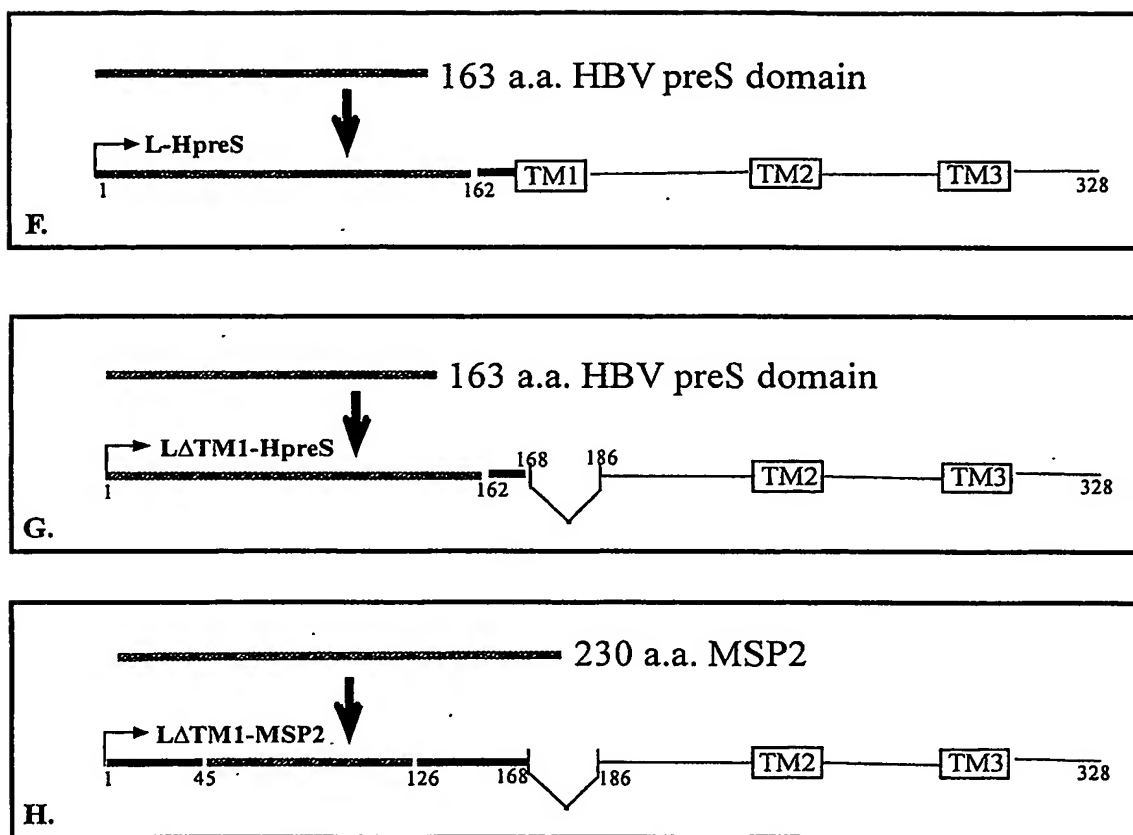


FIGURE 5 cont.

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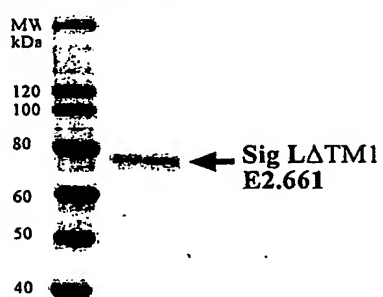
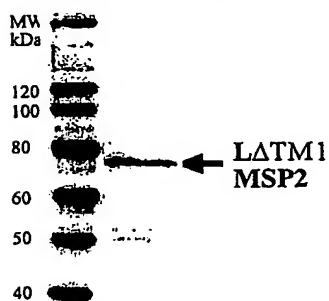
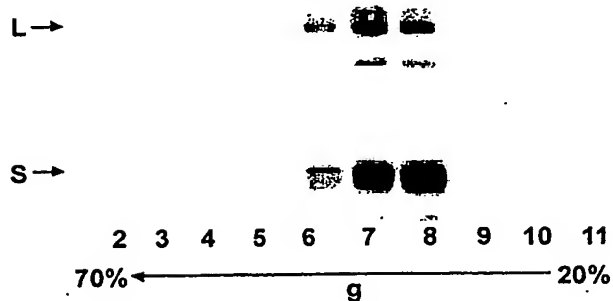
A. Sig Δ TM1-E2.661 membrane fractionB. Δ TM1-MSP2 membrane fraction

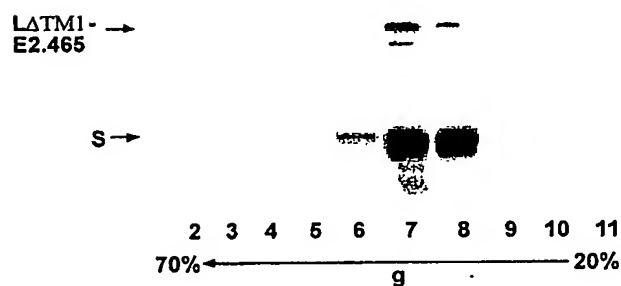
FIGURE 6

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A. DL/S VLPs: sucrose step gradient profile



B. DLATM1-E2.465 VLPs: sucrose step gradient profile



C. DLATM1-HpreS VLPs: sucrose step gradient profile

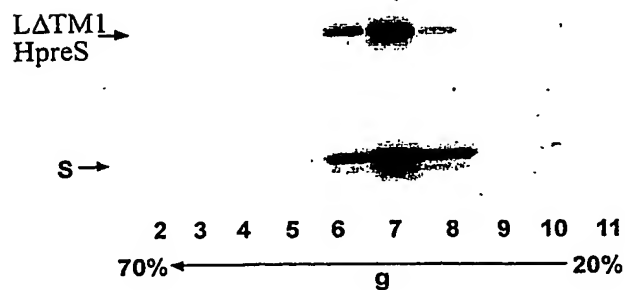
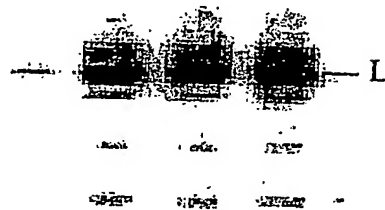


FIGURE 7

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rat sera:sequential bleeds
pre 1 2 4 5



preS reactivity

FIGURE 8